SEQUENCE LISTING

- <110> UNIVERSITÉ DE MONTREAL
- <120> NEW METALLOPROTEASES OF THE NEPRILYSIN FAMILY
- <130> BIOMEP INC. NEPRILYSIN
- <140> PCT/CA/00/00147
- <141> 2000-02-11
- <150> 2,260,376
- <151> 1999-02-11
- <160> 17
- <170> PatentIn Ver. 2.1
- <210> 1
- <211> 750
- <212> PRT
- <213> Homo sapiens
- <400> 1
- Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro 1 5 10 15
- Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser 20 25 30
- Val Leu Val Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu 35 40 45
- Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys
 50 60
- Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys 65 70 75 80
- Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val 85 90 95
- Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp 100 105 110
- Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu 115 120 125
- Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile 130 135 140
- Asn Glu Ser Ala Ile Asp Ser Arg Gly Glu Pro Leu Leu Lys Leu 145 150 155 160
- Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln 165 170 175

Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn 180 185 190

Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp 195 200 205

Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu 210 215 220

Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu 225 230 235 240

Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile 245 250 255

Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu 260 265 270

Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala 275 280 285

Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr 290 . 295 300

Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro 305 310 315 320

Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile 325 330 335

Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu 340 345 350

Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln 355 360 365

Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser 370 380

Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly 385 390 395

Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn 405 410 415

Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe 420 425 430

Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg

Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu 450 455 460

Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile 465 470 475 480

Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu 485 490 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile 500 505 510

Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu 515 520 525

Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala 530 535 540

Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu 545 550 550 560

Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly 565 570 575

Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp 580 585 590

Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr 595 600 605

Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr 610 615 620

Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn 625 630 635 640

Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
645 650 655

Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu 660 665 670

Lys Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu 675 680 685

Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val 690 695 700

Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile 705 710 715 720

Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
725 730 735

Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
740 745 750

<210> 2

<211> 749

<212> PRT

<213> Homo sapiens

Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn 1 5 10 15

Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val 20 25 30

Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln 35 40 45

Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala 50 55 60

Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe 65 70 75 80

Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu 85 90 95

Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp 100 105 110

Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp 115 120 125

Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn 130 135

Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu 145 150 155 160

Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro. 175

Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala 180 185 190

Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val 195 200 205

Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln 210 215 220

Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr 225 230 235 240

Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr 245 250 255

Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
260 265 270

Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His 275 280 285

Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu 290 295 300 Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys 305 310 315 320

Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser 325 330 335

Glu Asn Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg 340 345 350

Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Ala Asn Tyr Leu Val Trp 355 360 365

Arg Met Val Tyr Ser Arg Île Pro Asn Leu Ser Arg Arg Phe Gln Tyr 370 375 380

Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu 385 390 395 400

Pro Gln Trp Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr 405 410 415

Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys 420 425 430

Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp 435 440 445

Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys 450 455 460

Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro Glu 465 470 475 480

Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile Lys 485 490 495

Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys Tyr 500 505 510

Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr 515 520 525

Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser 530 540

Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe 545 550 555 560

Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val
565 570 575

Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys
580 585 590

Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu
595 600 605

Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn 610 615 620

Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr Leu 625 630 635 640

Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg Ala 645 650 655

Tyr Arg Lys Trp Ile Asn Asp Arg Gln Gly Leu Glu Glu Pro Leu 660 665 670

Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser Tyr 675 680 685

Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu Gln 690 695 700

Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly Ala 705 710 715 720

Ile Ser Asn Phe Glu Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro Asn 725 730 735

Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu Trp
740 745

<210> 3

<211> 732

<212> PRT

<213> Homo sapiens

<400> 3

Met Glu Gly Gly Asp Gln Ser Glu Glu Glu Pro Arg Glu Arg Ser Gln 1 5 10 15

Ala Gly Gly Met Gly Thr Leu Trp Ser Gln Glu Ser Thr Pro Glu Glu 20 25 30

Arg Leu Pro Val Glu Gly Ser Arg Pro Trp Ala Val Ala Arg Arg Val
35 40 45

Leu Thr Ala Ile Leu Ile Leu Gly Leu Leu Cys Phe Ser Val Leu 50 60

Leu Phe Tyr Asn Phe Gln Asn Cys Gly Pro Arg Pro Cys Glu Thr Ser
65 70 75 80

Val Cys Leu Asp Leu Arg Asp His Tyr Leu Ala Ser Gly Asn Thr Ser

Val Ala Pro Cys Thr Asp Phe Phe Ser Phe Ala Cys Gly Arg Ala Lys
100 105 110

Glu Thr Asn Asn Ser Phe Gln Glu Leu Ala Thr Lys Asn Lys Asn Arg

115 120 125 Leu Arg Arg Ile Leu Glu Val Gln Asn Ser Trp His Pro Gly Ser Gly Glu Glu Lys Ala Phe Gln Phe Tyr Asn Ser Cys Met Asp Thr Leu Ala 155 Ile Glu Ala Ala Gly Thr Gly Pro Leu Arg Gln Val Ile Glu Glu Leu Gly Gly Trp Arg Ile Ser Gly Lys Trp Thr Ser Leu Asn Phe Asn Arg 185 Thr Leu Arg Leu Leu Met Ser Gln Tyr Gly His Phe Pro Phe Phe Arg 200 Ala Tyr Leu Gly Pro His Pro Ala Ser Pro His Thr Pro Val Ile Gln 215 Ile Asp Gln Pro Glu Phe Asp Val Pro Leu Lys Gln Asp Gln Glu Gln 230 Lys Ile Tyr Ala Gln Ile Phe Arg Glu Tyr Leu Thr Tyr Leu Asn Gln 250 Leu Gly Thr Leu Leu Gly Gly Asp Pro Ser Lys Val Gln Glu His Ser 265 270 Ser Leu Ser Ile Ser Ile Thr Ser Arg Leu Phe Gln Phe Leu Arg Pro 280 Leu Glu Gln Arg Arg Ala Gln Gly Lys Leu Phe Gln Met Val Thr Ile 290 Asp Gln Leu Lys Glu Met Ala Pro Ala Ile Asp Trp Leu Ser Cys Leu 310 Gln Ala Thr Phe Thr Pro Met Ser Leu Ser Pro Ser Gln Ser Leu Val Val His Asp Val Glu Tyr Leu Lys Asn Met Ser Gln Leu Val Glu Glu Met Leu Lys Gln Arg Asp Phe Leu Gln Ser His Met Ile Leu Gly Leu Val Val Thr Leu Ser Pro Ala Leu Asp Ser Gln Phe Gln Glu Ala 375 Arg Arg Lys Leu Ser Gln Lys Leu Arg Glu Leu Thr Glu Gln Pro Pro 390 Met Pro Ala Arg Pro Arg Trp Met Lys Cys Val Glu Glu Thr Gly Thr

Phe Phe Glu Pro Thr Leu Ala Ala Leu Phe Val Arg Glu Ala Phe Gly

Pro Ser Thr Arg Ser Ala Ala Met Lys Leu Phe Thr Ala Ile Arg Asp 440 Ala Leu Ile Thr Arg Leu Arg Asn Leu Pro Trp Met Asn Glu Glu Thr Gln Asn Met Ala Gln Asp Lys Val Ala Gln Leu Gln Val Glu Met Gly Ala Ser Glu Trp Ala Leu Lys Pro Glu Leu Ala Arg Gln Glu Tyr Asn Asp Ile Gln Leu Gly Ser Ser Phe Leu Gln Ser Val Leu Ser Cys Val Arg Ser Leu Arg Ala Arg Ile Val Gln Ser Phe Leu Gln Pro His Pro 520 Gln His Arg Trp Lys Val Ser Pro Trp Asp Val Asn Ala Tyr Tyr Ser 535 Val Ser Asp His Val Val Phe Pro Ala Gly Leu Leu Gln Pro Pro 550 555 Phe Phe His Pro Gly Tyr Pro Arg Ala Val Asn Phe Gly Ala Ala Gly 570 Ser Ile Met Ala His Glu Leu Leu His Ile Phe Tyr Gln Leu Leu Leu Pro Gly Gly Cys Leu Ala Cys Asp Asn His Ala Leu Gln Glu Ala His Leu Cys Leu Lys Arg His Tyr Ala Ala Phe Pro Leu Pro Ser Arg Thr 615 Ser Phe Asn Asp Ser Leu Thr Phe Leu Glu Asn Ala Ala Asp Val Gly 625 Gly Leu Ala Ile Ala Leu Gln Ala Tyr Ser Lys Arg Leu Leu Arg His His Gly Glu Thr Val Leu Pro Ser Leu Asp Leu Ser Pro Gln Gln Ile Phe Phe Arg Ser Tyr Ala Gln Val Met Cys Arg Lys Pro Ser Pro Gln 680 Asp Ser His Asp Thr His Ser Pro Pro His Leu Arg Val His Gly Pro 695 Leu Ser Ser Thr Pro Ala Phe Ala Arg Tyr Phe Arg Cys Ala Arg Gly 710 715 Ala Leu Leu Asn Pro Ser Ser Arg Cys Gln Leu Trp

725 730

<210> 4 <211> 753 <212> PRT <213> Homo sapiens <400> 4

Met Ser Thr Tyr Lys Arg Ala Thr Leu Asp Glu Glu Asp Leu Val Asp

Ser Leu Ser Glu Gly Asp Ala Tyr Pro Asn Gly Leu Gln Val Asn Phe 20 25 30

His Ser Pro Arg Ser Gly Gln Arg Cys Trp Ala Ala Arg Thr Gln Val 35 40 45

Glu Lys Arg Leu Val Val Leu Val Leu Leu Ala Ala Gly Leu Val
50 60

Ala Cys Leu Ala Ala Leu Gly Ile Gln Tyr Gln Thr Arg Ser Pro Ser 65 70 75 80

Val Cys Leu Ser Glu Ala Cys Val Ser Val Thr Ser Ser Ile Leu Ser 85 90 95

Ser Met Asp Pro Thr Val Asp Pro Cys His Asp Phe Phe Ser Tyr Ala 100 105 110

Cys Gly Gly Trp Ile Lys Ala Asn Pro Val Pro Asp Gly His Ser Arg 115 120 125

Trp Gly Thr Phe Ser Asn Leu Trp Glu His Asn Gln Ala Ile Ile Lys 130 135

His Leu Leu Glu Asn Ser Thr Ala Ser Val Ser Glu Ala Glu Arg Lys 145 150 155 160

Ala Gln Val Tyr Tyr Arg Ala Cys Met Asn Glu Thr Arg Ile Glu Glu 165 170 175

Leu Arg Ala Lys Pro Leu Met Glu Leu Ile Glu Arg Leu Gly Gly Trp 180 185 190

Asn Ile Thr Gly Pro Trp Ala Lys Asp Asn Phe Gln Asp Thr Leu Gln

Val Val Thr Ala His Tyr Arg Thr Ser Pro Phe Phe Ser Val Tyr Val 210 215 220

Ser Ala Asp Ser Lys Asn Ser Asn Ser Asn Val Ile Gln Val Asp Gln 225 230 235 240

Ser Gly Leu Gly Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Lys Thr Glu 245 250 255 Asn Glu Lys Val Leu Thr Gly Tyr Leu Asn Tyr Met Val Gln Leu Gly 260 265 270

Lys Leu Gly Gly Gly Asp Glu Glu Ala Ile Arg Pro Gln Met Gln 275 280 285

Gln Ile Leu Asp Phe Glu Thr Ala Leu Ala Asn Ile Thr Ile Pro Gln 290 295 300

Glu Lys Arg Arg Asp Glu Glu Leu Ile Tyr His Lys Val Thr Ala Ala 305 310 315 320

Glu Leu Gln Thr Leu Ala Pro Ala Ile Asn Trp Leu Pro Phe Leu Asn 325 330 335

Thr Ile Phe Tyr Pro Val Glu Ile Asn Glu Ser Glu Pro Ile Val Val 340 345 350

Tyr Asp Lys Glu Tyr Leu Glu Gln Ile Ser Thr Leu Ile Asn Thr Thr 355 360 365

Asp Arg Cys Leu Leu Asn Asn Tyr Met Ile Trp Asn Leu Val Arg Lys 370 . 375 380

Thr Ser Ser Phe Leu Asp Gln Arg Phe Gln Asp Ala Asp Glu Lys Phe 385 390 395 400

Met Glu Val Met Tyr Gly Thr Lys Lys Thr Cys Leu Pro Arg Trp Lys 405 410 415

Phe Cys Val Ser Asp Thr Glu Asn Asn Leu Gly Phe Ala Leu Gly Pro 420 425 430

Met Phe Val Lys Ala Thr Phe Ala Glu Asp Ser Lys Ser Ile Ala Thr 435 440 445

Glu Ile Ile Leu Glu Ile Lys Lys Ala Phe Glu Glu Ser Leu Ser Thr 450 455 460

Leu Lys Trp Met Asp Glu Glu Thr Arg Lys Ser Ala Lys Glu Lys Ala 465 470 475 480

Asp Ala Ile Tyr Asn Met Ile Gly Tyr Pro Asn Phe Ile Met Asp Pro 485 490 495

Lys Glu Leu Asp Lys Val Phe Asn Asp Tyr Thr Ala Val Pro Asp Leu 500 505 510

Tyr Phe Glu Asn Ala Met Arg Phe Phe Asn Phe Ser Trp Arg Val Thr 515 520 525

Ala Asp Gln Leu Arg Lys Ala Pro Asn Arg Asp Gln Trp Ser Met Thr 530 540

Pro Pro Met Val Asn Ala Tyr Tyr Ser Pro Thr Lys Asn Glu Ile Val 545 550 555 560

Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Thr Arg Ser Ser Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val Val Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Asp Gly Asn 600 Leu Arg Pro Trp Trp Lys Asn Ser Ser Val Glu Ala Phe Lys Arg Gln 615 Thr Glu Cys Met Val Glu Gln Tyr Ser Asn Tyr Ser Val Asn Gly Glu 630 635 Pro Val Asn Gly Arg His Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly 650 Gly Leu Lys Ala Ala Tyr Arg Ala Tyr Gln Asn Trp Val Lys Lys Asn 660 Gly Ala Glu His Ser Leu Pro Thr Leu Gly Leu Thr Asn Asn Gln Leu Phe Phe Leu Gly Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His Glu Gly Leu Ile Thr Asp Pro His Ser Pro Ser Arg Phe 710 Arg Val Ile Gly Ser Leu Ser Asn Ser Lys Glu Phe Ser Glu His Phe 730 Arg Cys Pro Pro Gly Ser Pro Met Asn Pro Pro His Lys Cys Glu Val

Trp

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (14)
<223> i
<220>
<221> modified_base
<222> (18)
<223> i
<220>
<221> modified_base
<222> (18)
<223> i

```
<222> (21)
<223> i
<220>
<223> Description of Artificial Sequence:Oligonucleotide
      primers for RT-PCR reactions
<400> 5
tggatggatc gacngganac naca
                                                                     24
<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<221> modified base
<222> (14)
<223> i
<220>
<221> modified_base
<222> (18)
<223> i
<220>
<221> modified base
<222> (21)
<223> i
<223> Description of Artificial Sequence:Oligonucleotide
      primers for RT-PCR reactions
<400> 6
tggatggatc gacngganac nacg
                                                                     24
<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (4)
<223> i
<220>
<221> modified base
<222> (7)
<223> i
<220>
<221> modified_base
```

<222> (14)

```
<220>
<221> modified_base
<222> (17)
<223> i
<220>
<221> modified_base
<222> (20)
<223> i
<220>
<221> modified_base
<222> (25)
<223> i
<220>
<223> Description of Artificial Sequence:Oligonucleotide
      primers for RT-PCR reactions
<400> 7
agtngtnttt cccngcnggn_agtancttat ca
<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<221> modified base
<222> (4)
<223> i
<220>
<221> modified_base
<222> (7)
<223> i
<220>
<221> modified_base
<222> (14)
<223> i
<220>
<221> modified_base
<222> (17)
<223> i
<220>
<221> modified_base
<222> (20)
<223> i
<220>
```

<223> i

<221> modified_base

```
<222> (25)
<223> i
<220>
<223> Description of Artificial Sequence:
      Oligonucleotide primers for RT-PCR reactions
agtngtnttt cccngcnggn agtancttgc ca
                                                                     32
<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence
<220>
<221> modified_base
<222> (2)
<223> i
<220>
<221> modified_base
<222> (6)
<223> i
<220>
<221> modified base
<222> (9)
<223> i
<220>
<221> modified base
<222> (18)
<223> i
<220>
<221> modified_base
<222> (21)
<223> i
<220>
<223> Description of Artificial Sequence:Oligonucleotide
     primers for RT-PCR reactions
<220>
<221> modified_base
<222> (3)
<223> i
annecneena tetagtenge ngaetagttt etc
                                                                     33
<210> 10
<211> 35
```

<212> DNA

```
<220>
<221> modified_base
<222> (12)
<223> i
<220>
<221> modified_base
<222> (24)
<223> i
<220>
<223> Description of Artificial Sequence:Oligonucleotide
      primers for RT-PCR reactions
<400> 10
gatcaatctc tngatcgaag tctnaatctg gatgg
                                                                    35
<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence
<220>
<221> modified base
<222> (9)
<223> i
<220>
<221> modified_base
<222> (12)
<223> i
<220>
<221> modified_base
<222> (31)
<223> i
<220>
<223> Description of Artificial Sequence:Oligonucleotide
      primers for RT-PCR reactions
                                                                    37
tctcaccana tnctgagcat cgttcttcat ngggatg
<210> 12
<211> 2925
<212> DNA
<213> Mus musculus
<220>
<221> CDS
```

<213> Artificial Sequence

<222> (332)..(2626)

<400> 12 egggagecag cacegtgtga ceteacacee ageteagetg etetaeteea eeeggageee 60 accttggcca gctcacccca actctgagac atcccaacct agcctttaaq qacttgccta 120 gcagtgactg agagcaccag ggtcccctgg gcacttgggg cacagcttac agcattgaga 180 gcagagacca ggacagtgca ccagcttcag tgtgtcctag gcatccgatc cgggctccag 240 ctgcctctct cctagccctg gcctgggggg cttagcggtg tgccttccac ccagaaccgg 300 ctgataggga aagtctgaga gcccagtggg g atg gtg gag aga gca ggc tgg Met Val Glu Arg Ala Gly Trp tgt cgg aag aag tcc cca ggc ttc gtg gag tat ggg ctg atg gtg ctg 400 Cys Arg Lys Lys Ser Pro Gly Phe Val Glu Tyr Gly Leu Met Val Leu ctg ctg ctg ctg gga gcc ata gtg act ctg ggt gtc ttc tac agc 448 Leu Leu Leu Leu Gly Ala Ile Val Thr Leu Gly Val Phe Tyr Ser 30 35 ata ggg aag cag ctc ctc tta act agc ctg cta cac ttc tcc tgg 496 Ile Gly Lys Gln Leu Pro Leu Leu Thr Ser Leu Leu His Phe Ser Trp 40 gat gag agg acg gtt gta aaa cga gcc ctc agg gat tca tca ctg aaa Asp Glu Arg Thr Val Val Lys Arg Ala Leu Arg Asp Ser Ser Leu Lys agt gac atc tgc acc acc cca agc tgt gtg ata gca gct gcc aga atc 592 Ser Asp Ile Cys Thr Thr Pro Ser Cys Val Ile Ala Ala Ala Arg Ile ctc gaa aac atg gac caa tcg agg aac ccc tgt gaa aac ttc tac cag 640 Leu Glu Asn Met Asp Gln Ser Arg Asn Pro Cys Glu Asn Phe Tyr Gln 90 tac gcc tgc gga ggc tgg ctg agg cac cac gtg atc cca gag acc aac Tyr Ala Cys Gly Gly Trp Leu Arg His His Val Ile Pro Glu Thr Asn 105 tcc cga tac agc gtc ttt gac atc ctg cgg gac gag ctg gag gtt atc 736 Ser Arg Tyr Ser Val Phe Asp Ile Leu Arg Asp Glu Leu Glu Val Ile 120 135 ctc aaa ggg gtg ctg gag gat tcc act tcc cag cat cgc ccg gcc gtg 784 Leu Lys Gly Val Leu Glu Asp Ser Thr Ser Gln His Arg Pro Ala Val 140 150 gag aag goc aag aca cta tat ogc too tgc atg aac caa agt gtg atc 832 Glu Lys Ala Lys Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile 155 160 gag aag aga gac tot gag ooc otg otg ago gto tta aaa atg gta gga Glu Lys Arg Asp Ser Glu Pro Leu Leu Ser Val Leu Lys Met Val Gly

ggt tgg cct gtg gcc atg gat aag tgg aac gag acc atg ggc ctc aag 928 Gly Trp Pro Val Ala Met Asp Lys Trp Asn Glu Thr Met Gly Leu Lys 185 tgg gaa ctg gag cga cag ttg gct gtg ttg aac tcg cag ttc aac agg 976 Trp Glu Leu Glu Arg Gln Leu Ala Val Leu Asn Ser Gln Phe Asn Arg 205 egg gtc ctc atc gac ctc ttc atc tgg aat gac gac cag aac tcc agc 1024 Arg Val Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser egg cat gtc atc tac ata gac cag ecc acc ttg ggc atg eca tec egg 1072 Arg His Val Ile Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg gag tac tat ttc cag gag gac aac aac cac aag gta cgg aaa gcc tac 1120. Glu Tyr Tyr Phe Gln Glu Asp Asn Asn His Lys Val Arg Lys Ala Tyr ctg gag ttc atg acg tca gtg gcc act atg ctt agg aaa gac cag aac 1168 Leu Glu Phe Met Thr Ser Val Ala Thr Met Leu Arg Lys Asp Gln Asn 270 ctg tcc aag gag agc gcc atg gtg cgg gag gag atg gcg gag gtg ctg 1216 Leu Ser Lys Glu Ser Ala Met Val Arg Glu Glu Met Ala Glu Val Leu 285 290 gaa ctg gag acg cat ctg gcc aac gcc aca gtc ccc cag gag aaa agg 1264 Glu Leu Glu Thr His Leu Ala Asn Ala Thr Val Pro Gln Glu Lys Arg 305 cat gat gtc act gcc ctg tac cac cga atg gac ctg atg gag cta cag 1312 His Asp Val Thr Ala Leu Tyr His Arg Met Asp Leu Met Glu Leu Gln gaa agg ttt ggt ctg aag ggg ttt aac tgg act ctc ttc ata caa aac 1360 Glu Arg Phe Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Asn 330 335 gtg ttg tct tct gtg gaa gtc gag ctg ttc cca gat gag gag gtg gtg 1408 Val Leu Ser Ser Val Glu Val Glu Leu Phe Pro Asp Glu Glu Val Val 345 350 gto tac ggc atc ccc tac ctg gag aat ctg gag gat atc att gat agc 1456 Val Tyr Gly Ile Pro Tyr Leu Glu Asn Leu Glu Asp Ile Ile Asp Ser 360 365 tac toa goa ogg acc atg cag aac tac otg gta tgg ogc otg gtg ota 1504 Tyr Ser Ala Arg Thr Met Gln Asn Tyr Leu Val Trp Arg Leu Val Leu 380 385 gat cga att ggc agc ctg agc cag aga ttc aaa gag gcg cgt gtg gac 1552 Asp Arg Ile Gly Ser Leu Ser Gln Arg Phe Lys Glu Ala Arg Val Asp 395 400 405

										gta Val 420				1600	
									_	gcc Ala				1648	
1						-	_	_	_	agc Ser	_	_	_	1696	
										aac Asn				1744	
	_		 _	_	 _	_	-	_	_	cag Gln	_	_	_	1792	
										att Ile 500				1840	
										act Thr				1888	
Ī	_	_				_			_	aac Asn		_	_	1936	
										aat Asn				1984	
										aac Asn				2032	
		_		_		_	_			ttc Phe 580	_	_	-	2080	
	Gln									gtg Val				2128	
										ttt Phe				2176	
										cgg Arg				2224	

cag cag Gln Gln	tcg ca Ser Gl: 63	n Cys	atg Met	atc Ile	tat Tyr	cag Gln 640	tac Tyr	ggc Gly	aac Asn	ttc Phe	tct Ser 645	tgg Trp	gaa Glu	2272
	gac aa Asp As: 650													2320
att gcc Ile Ala 665	gac aa Asp As	c gga n Gly	ggt Gly	gtg Val 670	cga Arg	cag Gln	gca Ala	tac Tyr	aag Lys 675	gct Ala	tac Tyr	cta Leu	cgg Arg	2368
	gct ga Ala As													2416
	gcc ca Ala Gl													2464
	agg cc Arg Pr 71	o Glu												2512
agt cct Ser Pro	ctt aa Leu Ly 730	g tac s Tyr	agg Arg	gtg Val	ctg Leu 735	ggc Gly	tca Ser	cta Leu	cag Gln	aac Asn 740	ctg Leu	cca Pro	ggc Gly	2560
ttc tct Phe Ser 745	gag gc Glu Al	a ttc a Phe	cac His	tgc Cys 750	cca Pro	cga Arg	ggc Gly	agc Ser	ccc Pro 755	atg Met	cac His	ccc Pro	atg Met	2608
	tgt cg Cys Ar			tago	ccaa	ggc t	gag	ctate	gc tọ	gcgg	ccca	С		2656
gccccgc	cac cca	gaggct	it ag	gcgaa	atggi	t gta	agct	ggca	gaga	atgt	gca	ggtc	tttgcc	2716
tgaaggo	cac cgg	agccac	cc aç	gccag	gccc.	t ccg	gcgc	ccag	cct	agag	tgt	agcc	acccgc	2776
ccacacc	cgg gat	gagtgg	gt go	cggt	tcct	g cg	cccc	ctca	ggc	cagt	gag	ggtc	agcagc	2836
ccaggaa	igag cag	tcagct	g co	cttco	cacc	c tci	tcca	tagt	gtg	tggc	taa	atgt	tctcga	2896
gcttcag	act tga	gctaag	gt aa	acgo	cttc									2925

<210> 13

<211> 765

<212> PRT

<213 > Mus musculus

<400> 13

Met Val Glu Arg Ala Gly Trp Cys Arg Lys Lys Ser Pro Gly Phe Val

Glu Tyr Gly Leu Met Val Leu Leu Leu Leu Leu Gly Ala Ile Val

20

30

Thr Leu Gly Val Phe Tyr Ser Ile Gly Lys Gln Leu Pro Leu Leu Thr Ser Leu Leu His Phe Ser Trp Asp Glu Arg Thr Val Val Lys Arg Ala Leu Arg Asp Ser Ser Leu Lys Ser Asp Ile Cys Thr Thr Pro Ser Cys Val Ile Ala Ala Arg Ile Leu Glu Asn Met Asp Gln Ser Arg Asn Pro Cys Glu Asn Phe Tyr Gln Tyr Ala Cys Gly Gly Trp Leu Arg His His Val Ile Pro Glu Thr Asn Ser Arg Tyr Ser Val Phe Asp Ile Leu Arg Asp Glu Leu Glu Val Ile Leu Lys Gly Val Leu Glu Asp Ser Thr 135 Ser Gln His Arg Pro Ala Val Glu Lys Ala Lys Thr Leu Tyr Arg Ser 150 Cys Met Asn Gln Ser Val Ile Glu Lys Arg Asp Ser Glu Pro Leu Leu 170 Ser Val Leu Lys Met Val Gly Gly Trp Pro Val Ala Met Asp Lys Trp 180 Asn Glu Thr Met Gly Leu Lys Trp Glu Leu Glu Arg Gln Leu Ala Val 200 Leu Asn Ser Gln Phe Asn Arg Arg Val Leu Ile Asp Leu Phe Ile Trp 210 Asn Asp Asp Gln Asn Ser Ser Arg His Val Ile Tyr Ile Asp Gln Pro 230 Thr Leu Gly Met Pro Ser Arg Glu Tyr Tyr Phe Gln Glu Asp Asn Asn His Lys Val Arg Lys Ala Tyr Leu Glu Phe Met Thr Ser Val Ala Thr 265 Met Leu Arg Lys Asp Gln Asn Leu Ser Lys Glu Ser Ala Met Val Arg Glu Glu Met Ala Glu Val Leu Glu Leu Glu Thr His Leu Ala Asn Ala Thr Val Pro Gln Glu Lys Arg His Asp Val Thr Ala Leu Tyr His Arg 310 Met Asp Leu Met Glu Leu Gln Glu Arg Phe Gly Leu Lys Gly Phe Asn

325 335 Trp Thr Leu Phe Ile Gln Asn Val Leu Ser Ser Val Glu Val Glu Leu 345 Phe Pro Asp Glu Glu Val Val Tyr Gly Ile Pro Tyr Leu Glu Asn 360 Leu Glu Asp Ile Ile Asp Ser Tyr Ser Ala Arg Thr Met Gln Asn Tyr 375 Leu Val Trp Arg Leu Val Leu Asp Arg Ile Gly Ser Leu Ser Gln Arg Phe Lys Glu Ala Arg Val Asp Tyr Arg Lys Ala Leu Tyr Gly Thr Thr Val Glu Glu Val Arg Trp Arg Glu Cys Val Ser Tyr Val Asn Ser Asn Met Glu Ser Ala Val Gly Ser Leu Tyr Ile Lys Arg Ala Phe Ser Lys Asp Ser Lys Ser Thr Val Arg Glu Leu Ile Glu Lys Ile Arg Ser Val Phe Val Asp Asn Leu Asp Glu Leu Asn Trp Met Asp Glu Glu Ser Lys 470 475 Lys Lys Ala Gln Glu Lys Ala Met Asn Ile Arg Glu Gln Ile Gly Tyr 490 485 Pro Asp Tyr Ile Leu Glu Asp Asn Asn Lys His Leu Asp Glu Glu Tyr 505 Ser Ser Leu Thr Phe Tyr Glu Asp Leu Tyr Phe Glu Asn Gly Leu Gln 515 520 Asn Leu Lys Asn Asn Ala Gln Arg Ser Leu Lys Lys Leu Arg Glu Lys 535 Val Asp Gln Asn Leu Trp Ile Ile Gly Ala Ala Val Val Asn Ala Phe 545 Tyr Ser Pro Asn Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu Gln 570 Pro Pro Phe Phe Ser Lys Asp Gln Pro Gln Ser Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp Asn 600 Gly Arg Asn Phe Asp Lys Asn Gly Asn Met Leu Asp Trp Trp Ser Asn Phe Ser Ala Arg His Phe Gln Gln Gln Ser Gln Cys Met Ile Tyr Gln

635 640 630 625 Tyr Gly Asn Phe Ser Trp Glu Leu Ala Asp Asn Gln Asn Val Asn Gly 650 645 Phe Ser Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Arg Trp Leu Ala Asp Gly Gly Lys Asp Gln Arg Leu Pro Gly Leu Asn Leu Thr Tyr Ala Gln Leu Phe Phe Ile Asn Tyr Ala Gln Val Trp Cys Gly Ser Tyr Arg Pro Glu Phe Ala Val Gln Ser Ile Lys Thr Asp Val His Ser Pro Leu Lys Tyr Arg Val Leu Gly 730 Ser Leu Gln Asn Leu Pro Gly Phe Ser Glu Ala Phe His Cys Pro Arg 740 Gly Ser Pro Met His Pro Met Lys Arg Cys Arg Ile Trp 760 755 <210> 14 <211> 2676 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (7)..(2316) <400> 14 gtgggg atg gtg gag agc gcc ggc cgt gca ggg cag aag cgc ccg ggg 48 Met Val Glu Ser Ala Gly Arg Ala Gly Gln Lys Arg Pro Gly ttc ctg gag ggg ggg ctg ctg ctg ctg ctg ctg ctg gtg acc gct gcc 96 Phe Leu Glu Gly Gly Leu Leu Leu Leu Leu Leu Val Thr Ala Ala 15 ctg gtg gcc ttg ggt gtc ctc tac gcc gac cgc aga ggg aag cag ctg 144 Leu Val Ala Leu Gly Val Leu Tyr Ala Asp Arg Arg Gly Lys Gln Leu

cca cgc ctt gct agc cgg ctg tgc ttc tta cag gag gag agg acc ttt

Pro Arg Leu Ala Ser Arg Leu Cys Phe Leu Gln Glu Glu Arg Thr Phe

gta aaa cga aaa ccc cga ggg atc cca gag gcc caa gag gtg agc gag Val Lys Arg Lys Pro Arg Gly Ile Pro Glu Ala Gln Glu Val Ser Glu 70

50

65

192

gtc Val	tgc Cys 80	acc Thr	acc Thr	cct Pro	ggc Gly	tgc Cys 85	gtg Val	ata Ile	gca Ala	gcc Ala	gcc Ala 90	agg Arg	atc Ile	ctc Leu	cag Gln	288
aac Asn 95	atg Met	gac Asp	ccg Pro	acc Thr	acg Thr 100	gaa Glu	ccg Pro	tgt Cys	gac Asp	gac Asp 105	ttc Phe	tac Tyr	cag Gln	ttt Phe	gca Ala 110	336
tgc Cys	gga Gly	ggc Gly	tgg Trp	ctg Leu 115	cgg Arg	cgc Arg	cac His	gtg Val	atc Ile 120	cct Pro	gag Glu	acc Thr	aac Asn	tca Ser 125	aga Arg	384
tac Tyr	agc Ser	atc Ile	ttt Phe 130	gac Asp	gtc Val	ctc Leu	cgc Arg	gac Asp 135	gag Glu	ctg Leu	gag Glu	gtc Val	atc Ile 140	ctc Leu	aaa Lys	432
gcg Ala	gtg Val	ctg Leu 145	gag Glu	aat Asn	tcg Ser	act Thr	gcc Ala 150	aag Lys	gac Asp	cgg Arg	ccg Pro	gct Ala 155	gtg Val	gag Glu	aag Lys	480
gcc Ala	agg Arg 160	acg Thr	ctg Leu	tac Tyr	cgc Ar.g	tcc Ser 165	tgc Cys	atg Met	aac Asn	cag Gln	agt Ser 170	gtg Val	ata Ile	gag Glu	aag Lys	528
cga Arg 175	ggc Gly	tct Ser	cag Gln	ccc Pro	ctg Leu 180	ctg Leu	gac Asp	atc Ile	ttg Leu	gag Glu 185	gtg Val	gtg Val	gga Gly	ggc Gly	tgg Trp 190	576
ccg Pro	gtg Val	gcg Ala	atg Met	gac Asp 195	agg Arg	tgg Trp	aac Asn	gag Glu	acc Thr 200	gta Val	gga Gly	ctc Leu	gag Glu	tgg Trp 205	gag Glu	624
ctg Leu	gag Glu	cgg Arg	cag Gln 210	ctg Leu	gcg Ala	ctg Leu	atg Met	aac Asn 215	tca Ser	cag Gln	ttc Phe	aac Asn	agg Arg 220	cgc Arg	gtc Val	672
ctc Leu	atc Ile	gac Asp 225	ctc Leu	ttc Phe	atc Ile	tgg Trp	aac Asn 230	gac Asp	gac Asp	cag Gln	aac Asn	tcc Ser 235	agc Ser	cgg Arg	cac His	720
atc Ile	atc Ile 240	tac Tyr	ata Ile	gac Asp	cag Gln	ccc Pro 245	acc Thr	ttg Leu	ggc Gly	atg Met	ccc Pro 250	tcc Ser	cga Arg	gag Glu	tac Tyr	768
tac Tyr 255	ttc Phe	aac Asn	ggc Gly	ggc Gly	agc Ser 260	aac Asn	cgg Arg	aag Lys	gtg Val	cgg Arg 265	gaa Glu	gcc Ala	tac Tyr	ctg Leu	cag Gln 270	816
ttc Phe	atg Met	gtg Val	tca Ser	gtg Val 275	gcc Ala	acg Thr	ttg Leu	ctg Leu	cgg Arg 280	gag Glu	gat Asp	gca Ala	aac Asn	ctg Leu 285	ccc Pro	864
agg Arg	gac Asp	agc Ser	tgc Cys 290	ctg Leu	gtg Val	cag Gln	gag Glu	gac Asp 295	atg Met	gtg Val	cag Gln	gtt Val	ctg Leu 300	g a g Glu	ctg Leu	912

gag	aca	cag	ctg	gcc	aag	gcc	acg	gta	ccc	cag	gag	gag	aga	cac	gac	960	
Glu	Thr	Gln 305	Leu	Ala	Lys	Ala	Thr 310	Val	Pro	Gln	Glu	Glu 315	Arg	His	Asp		
gtc Val	atc Ile 320	gcc Ala	ttg Leu	tac Tyr	cac His	cgg Arg 325	atg Met	gga Gly	ctg Leu	gag Glu	gag Glu 330	ctg Leu	caa Gln	agc Ser	cag Gln	1008	
ttt Phe 335	ggc Gly	ctg Leu	aag Lys	gga Gly	ttt Phe 340	aac Asn	tgg Trp	act Thr	ctg Leu	ttc Phe 345	ata Ile	caa Gln	act Thr	gtg Val	cta Leu 350	1056	
				atc Ile 355												1104	
ggc Gly	atc Ile	ccc Pro	tac Tyr 370	ctg Leu	cag Gln	aac Asn	ctt Leu	gaa Glu 375	aac Asn	atc Ile	atc Ile	gac Asp	acc Thr 380	tac Tyr	tca Ser	1152	
gcc Ala	agg Arg	acc Thr 385	ata Ile	cag Gln	aac Asn	tac Tyr	ctg Leu 390	gtc Val	tgg Trp	cgc Arg	ctg Leu	gtg Val 395	ctg Leu	gac Asp	cgc Arg	1200	
att Ile	ggt Gly 400	agc Ser	cta Leu	agc Ser	cag Gln	aga Arg 405	ttc Phe	aag Lys	gac Asp	aca Thr	cga Arg 410	gtg Val	aac Asn	tac Tyr	cgc Arg	1248	
aag Lys 415	gcg Ala	ctg Leu	ttt Phe	ggc Gly	aca Thr 420	atg Met	gtg Val	gag Glu	gag Glu	gtg Val 425	cgc Arg	tgg Trp	cgt Arg	gaa Glu	tgt Cys 430	1296	
gtg Val	ggc Gly	tac Tyr	gtc Val	aac Asn 435	agc Ser	aac Asn	atg Met	gag Glu	aac Asn 440	gcc Ala	gtg Val	ggc Gly	tcc Ser	ctc Leu 445	tac Tyr	1344	
gtc Val	agg Arg	gag Glu	gcg Ala 450	ttc Phe	cct Pro	gga Gly	gac Asp	agc Ser 455	aag Lys	agc Ser	atg Met	gtc Val	aga Arg 460	gaa Glu	ctc Leu	1392	
				cgg Arg												1440	
tgg Trp	atg Met 480	gac Asp	gag Glu	gag Glu	tcc Ser	aag Lys 485	aag Lys	aag Lys	gcg Ala	cag Gln	gag Glu 490	aag Lys	gcc Ala	atg Met	agc Ser	1488	
atc Ile 495	cgg Arg	gag Glu	cag Gln	atc Ile	999 Gly 500	cac His	cct Pro	gac Asp	tac Tyr	atc Ile 505	ctg Leu	gag Glu	gag Glu	atg Met	aac Asn 510	1536	
agg Arg	cgc Arg	ctg Leu	gac Asp	gag Glu 515	gag Glu	tac Tyr	tcc Ser	aat Asn	ctg Leu 520	aac Asn	ttc Phe	tca Ser	gag Glu	gac Asp 525	ctg Leu	1584	
tac	ttt	gag	aac	agt	ctg	cag	aac	ctc	aag	gtg	ggc	gcc	cag	cgg	agc	1632	

Tyr	Phe	Glu	Asn 530	Ser	Leu	Gln	Asn	Leu 535	Lys	Val	Gly	Ala	Gln 540	Arg	Ser	
	agg Arg															1680
	gcg Ala 560		_		_								_			1728
	cct Pro															1776
-	gcc Ala															1824
	cac His															1872
	atg Met															1920
	gag Glu 640	_	_			_							_			1968
_	gaa Glu	-										_			_	2016
_	aac Asn						_									2064
	gag Glu															2112
	cag Gln															2160
	ccc Pro 720															2208
	aag Lys															2256
	acg Thr															2304

755 760 765

tgc cgc gtg tgg tagccaaggc cctgccgcgc tgtgcggccc acgcccaccc Cys Arg Val Trp 770 2356

gctgctcgga ggcatctgtg cgaaggtgca gctagcggcg acccagtgta cgtcccgccc 2416 cggccaacca tgccaagcct gcctgccagg cctctgcgcc tggcctaggg tgcagccacc 2476 tgcctgacac ccagggatga gcagtgtcca gtgcagtacc tggaccggag cccccttcac 2536 agacacccgc ggggctcagt gccccgtca caactctgta gagacaatca actgtgtcct 2596 gcccaccctt caaggtgcat tgtcttccag tatctacagc ttcagaactt gagctaagta 2656 aatgctttca aagaaaaaaa 2676

<210> 15

<211> 770

<212> PRT

<213> Homo sapiens

<400> 15

Met Val Glu Ser Ala Gly Arg Ala Gly Gln Lys Arg Pro Gly Phe Leu
1 5 10 15

Glu Gly Gly Leu Leu Leu Leu Leu Leu Val Thr Ala Ala Leu Val
20 25 30

Ala Leu Gly Val Leu Tyr Ala Asp Arg Arg Gly Lys Gln Leu Pro Arg
35 40 45

Leu Ala Ser Arg Leu Cys Phe Leu Gln Glu Glu Arg Thr Phe Val Lys
50 55 60

Arg Lys Pro Arg Gly Ile Pro Glu Ala Gln Glu Val Ser Glu Val Cys 65 70 75 80

Thr Thr Pro Gly Cys Val Ile Ala Ala Ala Arg Ile Leu Gln Asn Met 85 90 95

Asp Pro Thr Thr Glu Pro Cys Asp Asp Phe Tyr Gln Phe Ala Cys Gly
100 105 110

Gly Trp Leu Arg Arg His Val Ile Pro Glu Thr Asn Ser Arg Tyr Ser 115 120 125

Ile Phe Asp Val Leu Arg Asp Glu Leu Glu Val Ile Leu Lys Ala Val 130 135 140

Leu Glu Asn Ser Thr Ala Lys Asp Arg Pro Ala Val Glu Lys Ala Arg 145 150 155 160

Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile Glu Lys Arg Gly
165 170 175

Ser Gln Pro Leu Leu Asp Ile Leu Glu Val Val Gly Gly Trp Pro Val Ala Met Asp Arg Trp Asn Glu Thr Val Gly Leu Glu Trp Glu Leu Glu 200 Arq Gln Leu Ala Leu Met Asn Ser Gln Phe Asn Arg Arg Val Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser Arg His Ile Ile 230 Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg Glu Tyr Tyr Phe 250 Asn Gly Gly Ser Asn Arg Lys Val Arg Glu Ala Tyr Leu Gln Phe Met 265 Val Ser Val Ala Thr Leu Leu Arg Glu Asp Ala Asn Leu Pro Arg Asp 280 Ser Cys Leu Val Gln Glu Asp Met Val Gln Val Leu Glu Leu Glu Thr 295 Gln Leu Ala Lys Ala Thr Val Pro Gln Glu Glu Arg His Asp Val Ile 310 Ala Leu Tyr His Arg Met Gly Leu Glu Glu Leu Gln Ser Gln Phe Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Thr Val Leu Ser Ser 345 Val Lys Ile Lys Leu Pro Asp Glu Glu Val Val Tyr Gly Ile Pro Tyr Leu Gln Asn Leu Glu Asn Ile Ile Asp Thr Tyr Ser Ala Arg 375 Thr Ile Gln Asn Tyr Leu Val Trp Arg Leu Val Leu Asp Arg Ile Gly Ser Leu Ser Gln Arg Phe Lys Asp Thr Arg Val Asn Tyr Arg Lys Ala Leu Phe Gly Thr Met Val Glu Glu Val Arg Trp Arg Glu Cys Val Gly Tyr Val Asn Ser Asn Met Glu Asn Ala Val Gly Ser Leu Tyr Val Arg 440 Glu Ala Phe Pro Gly Asp Ser Lys Ser Met Val Arg Glu Leu Ile Asp 450 455 Lys Val Arg Thr Val Phe Val Glu Thr Leu Asp Glu Leu Gly Trp Met

470

465

Asp Glu Glu Ser Lys Lys Ala Gln Glu Lys Ala Met Ser Ile Arg 485 490 495

Glu Gln Ile Gly His Pro Asp Tyr Ile Leu Glu Glu Met Asn Arg Arg 500 505 510

Leu Asp Glu Glu Tyr Ser Asn Leu Asn Phe Ser Glu Asp Leu Tyr Phe 515 520 525

Glu Asn Ser Leu Gln Asn Leu Lys Val Gly Ala Gln Arg Ser Leu Arg 530 535 540

Lys Leu Arg Glu Lys Val Asp Pro Asn Leu Trp Ile Ile Gly Ala Ala 545 550 550 560

Val Val Asn Ala Phe Tyr Ser Pro Asn Arg Asn Gln Ile Val Phe Pro 565 570 575

Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Lys Glu Gln Pro Gln Ala 580 585 590

Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His 595 600 605

Gly Phe Asp Asp Asp Gly Arg Asp Phe Asp Lys Asp Gly Asp Met Met 610 615 620

Asp Trp Trp Ser Asn Phe Ser Thr Gln His Phe Arg Glu Gln Ser Glu 625 630 635 640

Cys Met Ile Tyr Gln Tyr Gly Asn Tyr Ser Trp Asp Leu Ala Asp Glu 645 650

Gln Asn Val Asn Gly Phe Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn 660 665 670

Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Lys Trp Met Ala Glu 675 680 685

Gly Gly Lys Asp Gln Gln Leu Pro Gly Leu Asp Leu Thr His Glu Gln 690 695 700

Leu Phe Phe Ile Asn Tyr Ala Gln Val Trp Cys Gly Ser Tyr Arg Pro 705 710 715 720

Glu Phe Ala Ile Gln Ser Ile Lys Thr Asp Val His Ser Pro Leu Lys
725 730 735

Tyr Arg Val Leu Gly Ser Leu Gln Asn Leu Ala Ala Phe Ala Asp Thr
740 745 750

Phe His Cys Ala Arg Gly Thr Pro Met His Pro Lys Glu Arg Cys Arg 755 760 765

Val Trp

<210> 16 <211> 2871 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (205)..(2529) <400> 16 cgacccgctc ggtcaccgcc ggctcgggcg cgcacctgcc ggctgcggcc ccagggccat 120 geggaggeee acgaggagge eggeggeeae gegeateeeg tageeeaggt ggeeeaggte 180 tgcaccgcgg cggcctcggc gccg atg gag ccc ccg tat tcg ctg acg gcg 231 Met Glu Pro Pro Tyr Ser Leu Thr Ala 279 cac tac gat gag ttc caa gag gtc aag tac gtg agc cgc tgc ggc gcg His Tyr Asp Glu Phe Gln Glu Val Lys Tyr Val Ser Arg Cys Gly Ala 10 15 ggg ggc gcg cgc ggg gcc tcc ctg ccc ccg ggc ttc ccg ttg ggc gct Gly Gly Ala Arg Gly Ala Ser Leu Pro Pro Gly Phe Pro Leu Gly Ala 375 geg ege age gee ace ggg gee egg tee ggg etg eeg ege tgg aac egg Ala Arg Ser Ala Thr Gly Ala Arg Ser Gly Leu Pro Arg Trp Asn Arg ege gag gtg tge etg etg teg ggg etg gtg tte gee gge ete tge 423 Arg Glu Val Cys Leu Leu Ser Gly Leu Val Phe Ala Ala Gly Leu Cys 60 65 gee att etg geg get atg etg gee ete aag tae etg gge eeg gte geg 471 Ala Ile Leu Ala Ala Met Leu Ala Leu Lys Tyr Leu Gly Pro Val Ala 75 519 gcc ggc ggc gcc tgt ccc gag ggc tgc cct gag cgc aag gcc ttc Ala Gly Gly Gly Ala Cys Pro Glu Gly Cys Pro Glu Arg Lys Ala Phe 90 105 567 geg ege gee get ege tte etg gee gee aac etg gae gee age ate gae Ala Arg Ala Arg Phe Leu Ala Ala Asn Leu Asp Ala Ser Ile Asp 110 120 115 615 Pro Cys Gln Asp Phe Tyr Ser Phe Ala Cys Gly Gly Trp Leu Arg Arg 125 130 135 cac gcc atc ccc gac gac aag ctc acc tat ggc acc atc gcg gca atc 663 His Ala Ile Pro Asp Asp Lys Leu Thr Tyr Gly Thr Ile Ala Ala Ile

140	145	150

					cgg Arg				711
					cgc Arg				759
_	_	_			gag Glu				807
					ggc Gly 210				855
					tgg Trp				903 ,
					gcc Ala				951
					cgc Arg				999
_				 	acc Thr				1047
					tac Tyr 290				1095
					gtg Val				1143
					aac Asn				1191
					atg Met				1239
					ttg Leu				1287
					gag Glu 370				1335

gcg Ala	aca Thr	gac Asp 380	tac Tyr	atg Met	cag Gln	cag Gln	gtg Val 385	tcg Ser	cag Gln	ctc Leu	atc Ile	cgc Arg 390	tcc Ser	aca Thr	ccc Pro	1383
		gtc Val														1431
		cac His														1479
		atg Met														1527
_		cag Gln	_		_				_				_			1575
_		gag Glu 460				-	_	_		_	_	-				1623
	_	gac Asp		_			_		_	_	_			_	_	1671
	_	gac Asp	_				-	_	_		_	_		_		1719
		gtg Val														1767
		aag Lys														1815
		ttg Leu 540														1863
		cag Gln														1911
									220	C 2 C	ato	ata	ttc	CCC	aca	1959
		gcc Ala														1333

aac tac ggg ggc a Asn Tyr Gly Gly I 605	tc ggc acc atc le Gly Thr Ile	att gga cat Ile Gly His 610	gag ctg acc cac ggc Glu Leu Thr His Gly 615	2055
		Asp Arg Ser	ggg aac ctg ctg cac Gly Asn Leu Leu His 630	2103
			cga aag gct gag tgc Arg Lys Ala Glu Cys 645	2151
	_	_	aac cag cgg gtg aac Asn Gln Arg Val Asn 665	2199
Gly Lys His Thr L			atg ggc ggc ctc aag Met Gly Gly Leu Lys 680	
			gag cac ggc cca gag Glu His Gly Pro Glu 695	2295
		Thr His Asp	cag ctc ttc ttc att Gln Leu Phe Phe Ile 710	2343
			tcg cag tcc atc tac Ser Gln Ser Ile Tyr 725	2391
			cac tac agg gtg ctg His Tyr Arg Val Leu 745	2439
Gly Ser Val Ser G			gtt tta cac tgt cca Val Leu His Cys Pro 760	2487
aag gtc tca ccc a Lys Val Ser Pro M 765				2529
tgaccctggc tgcccg	cctg cacgeeece	a ctgccccgc	acgaatcacc tcctgctggc	2589
taccggggca ggcatg	cacc cggtgccag	c cccgctctgg	gcaccacctg ccttccagcc	2649
cctccaggac ccggtc	cccc tgctgcccc	t cacttcagga	ggggcctgga gcagggtgag	2709
			cccagattct gctctaaggg	
			ttcgctgtgt tcttgctgca	
agtctggtca aataaa	tcac tgcactgtt	a aaaaaaaaa	aa	2871

-

. • • • · · · •

<210> 17

6 15

<211> 775

<212> PRT

<213> Homo sapiens

<400> 17

Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu 1 5 10 15

Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser 20 25 30

Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala 35 40 45

Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser 50 60

Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu 65 70 75 80

Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro 85 90 95

Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Arg Phe Leu 100 105 110

Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser 115 120 125

Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys 130 135 140

Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
145 150 155 160

Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala
165 170 175

Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu 180 185 190

Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
195 200 205

Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala 210 215 220

Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser 225 230 235 240

Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser 245 250 255

Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu 260 265 270 Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Val Leu Ala 275 280 285

Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp 290 295 300

Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu 305 310 315 320

Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser 325 330 335

Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro 340 345 350

His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe 355 360 365

Ser Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln 370 375 380

Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr 385 390 395 400

Leu Val Trp Arg Val Val Val Leu Ser Glu His Leu Ser Pro Pro 405 410 415

Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp 420 425 430

Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His 435 440 445

Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala 450 455 460

Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile 465 470 475 480

Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg 485 490 495

Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
500 505 510

Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe 515 520 525

Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg 530 535 540

Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys 545 550 555 560

Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro 565 570 575

Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu 580 585 590

Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr 595 600 605

Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gln 610 615 620

Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr 625 630 635 640

Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn 645 650 655

Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu 660 665 670

Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln 675 680 685

Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys 690 695 700

Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys 705 710 715 720

Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys 725 730 735

His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu 740 745 750

Glu Phe Gly Arg Val Leu His Cys Pro Lys Val Ser Pro Met Asn Pro 755 760 765

Ala His Lys Cys Ser Val Trp
770 775